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RAW SEQUENCE LISTING DATE: 11/29/2002
PATENT APPLICATION: **US/09/884,319** TIME: 16:01:32

Input Set : **N:\Crf3\RULE60\09884319.raw**
Output Set: **N:\CRF4\11292002\I884319.raw**

SEQUENCE LISTING

(1) GENERAL INFORMATION:
(i) APPLICANT: Lin, Lih-Ling
Graham, James
(ii) TITLE OF INVENTION: NOVEL INTERLEUKIN-1 RECEPTOR INTRACELLULAR LIGAND PROTEINS AND INHIBITORS OF LIGAND BINDING
(iii) NUMBER OF SEQUENCES: 7
(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.
(B) STREET: 87 CambridgePark Drive
(C) CITY: Cambridge
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02140
(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
(vi) CURRENT APPLICATION DATA:
C--> **(A) APPLICATION NUMBER: US/09/884,319**
C--> **(B) FILING DATE: 18-Jun-2001**
(C) CLASSIFICATION:
(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US/09/083,516
(B) FILING DATE:
(A) APPLICATION NUMBER: 08/487,942
(B) FILING DATE:
(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Brown, Scott A.
(B) REGISTRATION NUMBER: 32,724
(C) REFERENCE/DOCKET NUMBER: GI5258
(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (617) 498-8224
(B) TELEFAX: (617) 876-5851
(2) INFORMATION FOR SEQ ID NO: 1:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1571 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA

ENTERED

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PATENT APPLICATION: **US/09/884,319** TIME: 16:01:32

Input Set : **N:\Crf3\RULE60\09884319.raw**
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60    (iii) HYPOTHETICAL: NO
63     (ix) FEATURE:
64           (A) NAME/KEY: CDS
65           (B) LOCATION: 2..529
68     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
70 G ATC CCC AGG GTG GAC CTC CGG GTG TGG CAG GAC TGC TGT GAA GAC          46
71   Ile Pro Arg Val Asp Leu Arg Val Trp Gln Asp Cys Cys Glu Asp
72     1               5                  10                  15
74 TGT AGG ACC AGG GGG CAG TTC AAT GCC TTT TCC TAT CAT TTC CGA GGC         94
75 Cys Arg Thr Arg Gly Gln Phe Asn Ala Phe Ser Tyr His Phe Arg Gly
76                  20                  25                  30
78 AGA CGG TCT CTT GAG TTC AGC TAC CAG GAG GAC AAG CCG ACC AAG AAA        142
79 Arg Arg Ser Leu Glu Phe Ser Tyr Gln Glu Asp Lys Pro Thr Lys Lys
80              35                  40                  45
82 ACA AGA CCA CGG AAA ATA CCC AGT GTT GGG AGA CAG GGG GAA CAT CTC        190
83 Thr Arg Pro Arg Lys Ile Pro Ser Val Gly Arg Gln Gly Glu His Leu
84          50                  55                  60
86 AGC AAC AGC ACC TCA GCC TTC AGC ACA CGC TCA GAT GCA TCT GGG ACA        238
87 Ser Asn Ser Thr Ser Ala Phe Ser Thr Arg Ser Asp Ala Ser Gly Thr
88      65                  70                  75
90 AAT GAC TTC AGA GAG TTT GTT CTG GAA ATG CAG AAG ACC ATC ACA GAC        286
91 Asn Asp Phe Arg Glu Phe Val Leu Glu Met Gln Lys Thr Ile Thr Asp
92  80                  85                  90                  95
94 CTC AGA ACA CAG ATA AAG AAA CTT GAA TCA CGG CTC AGT ACC ACA GAG        334
95 Leu Arg Thr Gln Ile Lys Lys Leu Glu Ser Arg Leu Ser Thr Thr Glu
96                  100                 105                 110
98 TGC GTG GAT GCC GGG GGC GAA TCT CAC GCC AAC AAC ACC AAG TGG AAA        382
99 Cys Val Asp Ala Gly Gly Glu Ser His Ala Asn Asn Thr Lys Trp Lys
100             115                 120                 125
102 AAA GAT GCA TGC ACC ATT TGT GAA TGC AAA GAC GGG CAG GTC ACC TGC       430
103 Lys Asp Ala Cys Thr Ile Cys Glu Cys Lys Asp Gly Gln Val Thr Cys
104         130                 135                 140
106 TTC GTG GAA GCT TGC CCC CCT GCC ACC TGT GCT GTC CCC GTG AAC ATC       478
107 Phe Val Glu Ala Cys Pro Pro Ala Thr Cys Ala Val Pro Val Asn Ile
108     145                 150                 155
110 CCA GGG GCC TGC TGT CCA GTC TGC TTA CAG AAG AGG GCG GAG GAA AAG       526
111 Pro Gly Ala Cys Cys Pro Val Cys Leu Gln Lys Arg Ala Glu Glu Lys
112 160                 165                 170                 175
114 CCC TAGGCTCCTG GGAGGCTCCT CAGAGTTTGT CTGCTGTGCC ATCGTGAGAT            579
115 Pro
118 CGGGTGGCCG ATGGCAGGGA GCTGCGGACT GCAGACCAGG AAACACCCAG AACTCGTGAC     639
120 ATTTCATGAC AACGTCCAGC TGGTGCTGTT ACAGAAGGCA GTGCAGGAGG CTTCCAACCA     699
122 GAGCATCTGC GGAGAAGGAG GCACAGCAGG TGCCTGAAGG GAAGCAGGCA GGAGTCCTAG     759
124 CTTCACGTTA GACTTCTCAG GTTTTTATTT AATTCTTTTA AAATGAAAAA TTGGTGCTAC     819
126 TATTAAATTG CACAGTTGAA TCATTTAGGC GCCTAAATTG ATTTTGCCTC CCAACACCAT     879
128 TTCTTTTTAA ATAAAGCAGG ATACCTCTAT ATGTCAGCCT TGCCTTGTTC AGATGCCAGG     939
130 AGCCGGCAGA CCTGTCACCC GCAGGTGGGG TGAGTCTCGG AGCTGCCAGA GGGGCTCACC     999
132 GAAATCGGGG TTCCATCACA AGCTATGTTT AAAAAGAAAA TTGGTGTTTG CCAAACGGAA    1059
134 CAGAACCTTT GATGAGAGCG TTCACAGGGA CACTGTCTGG GGGTGCAGTG CAAGCCCCCG    1119
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Input Set : **N:\Crf3\RULE60\09884319.raw**
Output Set: **N:\CRF4\11292002\I884319.raw**

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136 GCCTCTTCCC TGGGAACCTC TGAACTCCTC CTTCCTCTGG GCTCTCTGTA ACATTTCACC    1179
138 ACACGTCAGC ATCTAATCCC AAGACAAACA TTCCCGCTGC TCGAAGCAGC TGTATAGCCT    1239
140 GTGACTCTCC GTGTGTCAGC TCCTTCCACA CCTGATTAGA ACATTCATAA GCCACATTTA    1299
142 GAAACAGGTT TGCTTTCAGC TGTCACTTGC ACACATACTG CCTAGTTGTG AACCAAATGT    1359
144 GAAAAAACCT CCTTCATCCC ATTGTGTATC TGATACCTGC CGAGGGCCAA GGGTGTGTGT    1419
146 TGACAACGCC GCTCCCAGCC GGCCCTGGTT GCGTCCACGT CCTGAACAAG AGCCGCTTCC    1479
148 GGATGGCTCT TCCCAAGGGA GGAGGAGCTC AAGTGTCGGG AACTGTCTAA CTTCAGGTTG    1539
150 TGTGAGTGCG TTAAAAAAAA AAAAAAAAAA AA                                  1571
153 (2) INFORMATION FOR SEQ ID NO: 2:
155      (i) SEQUENCE CHARACTERISTICS:
156           (A) LENGTH: 176 amino acids
157           (B) TYPE: amino acid
158           (D) TOPOLOGY: linear
160     (ii) MOLECULE TYPE: protein
162     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
164 Ile Pro Arg Val Asp Leu Arg Val Trp Gln Asp Cys Cys Glu Asp Cys
165   1               5                  10                  15
167 Arg Thr Arg Gly Gln Phe Asn Ala Phe Ser Tyr His Phe Arg Gly Arg
168              20                  25                  30
170 Arg Ser Leu Glu Phe Ser Tyr Gln Glu Asp Lys Pro Thr Lys Lys Thr
171          35                  40                  45
173 Arg Pro Arg Lys Ile Pro Ser Val Gly Arg Gln Gly Glu His Leu Ser
174      50                  55                  60
176 Asn Ser Thr Ser Ala Phe Ser Thr Arg Ser Asp Ala Ser Gly Thr Asn
177  65                  70                  75                  80
179 Asp Phe Arg Glu Phe Val Leu Glu Met Gln Lys Thr Ile Thr Asp Leu
180                  85                  90                  95
182 Arg Thr Gln Ile Lys Lys Leu Glu Ser Arg Leu Ser Thr Thr Glu Cys
183              100                 105                 110
185 Val Asp Ala Gly Gly Glu Ser His Ala Asn Asn Thr Lys Trp Lys Lys
186          115                 120                 125
188 Asp Ala Cys Thr Ile Cys Glu Cys Lys Asp Gly Gln Val Thr Cys Phe
189      130                 135                 140
191 Val Glu Ala Cys Pro Pro Ala Thr Cys Ala Val Pro Val Asn Ile Pro
192 145                 150                 155                 160
194 Gly Ala Cys Cys Pro Val Cys Leu Gln Lys Arg Ala Glu Glu Lys Pro
195                 165                 170                 175
198 (2) INFORMATION FOR SEQ ID NO: 3:
200      (i) SEQUENCE CHARACTERISTICS:
201           (A) LENGTH: 1088 base pairs
202           (B) TYPE: nucleic acid
203           (C) STRANDEDNESS: double
204           (D) TOPOLOGY: linear
206     (ii) MOLECULE TYPE: cDNA
208    (iii) HYPOTHETICAL: NO
211     (ix) FEATURE:
212           (A) NAME/KEY: CDS
213           (B) LOCATION: 2..961
216     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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RAW SEQUENCE LISTING DATE: 11/29/2002
PATENT APPLICATION: **US/09/884,319** TIME: 16:01:32

Input Set : **N:\Crf3\RULE60\09884319.raw**
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```
218 G AAA AAA GGA GGT AAA ACA GAA CAG GAT GGC TAT CAG AAA CCC ACC          46
219   Lys Lys Gly Gly Lys Thr Glu Gln Asp Gly Tyr Gln Lys Pro Thr
220     1               5                  10                  15
222 AAC AAA CAC TTC ACG CAG AGT CCC AAG AAG TCA GTG GCC GAC CTG CTG          94
223 Asn Lys His Phe Thr Gln Ser Pro Lys Lys Ser Val Ala Asp Leu Leu
224                 20                  25                  30
226 GGG TCC TTT GAA GGC AAA CGA AGA CTC CTT CTG ATC ACT GCT CCC AAG         142
227 Gly Ser Phe Glu Gly Lys Arg Arg Leu Leu Leu Ile Thr Ala Pro Lys
228              35                  40                  45
230 GCT GAG AAC AAT ATG TAT GTG CAA CAA CGT GAT GAA TAT CTG GAA AGT         190
231 Ala Glu Asn Asn Met Tyr Val Gln Gln Arg Asp Glu Tyr Leu Glu Ser
232          50                  55                  60
234 TTC TGC AAG ATG GCT ACC AGG AAA ATC TCT GTG ATC ACC ATC TTC GGC         238
235 Phe Cys Lys Met Ala Thr Arg Lys Ile Ser Val Ile Thr Ile Phe Gly
236      65                  70                  75
238 CCT GTC AAC AAC AGC ACC ATG AAA ATC GAC CAC TTT CAG CTA GAT AAT         286
239 Pro Val Asn Asn Ser Thr Met Lys Ile Asp His Phe Gln Leu Asp Asn
240  80                  85                  90                  95
242 GAG AAG CCC ATG CGA GTG GTG GAT GAT GAA GAC TTG GTA GAC CAG CGT         334
243 Glu Lys Pro Met Arg Val Val Asp Asp Glu Asp Leu Val Asp Gln Arg
244                 100                 105                 110
246 CTC ATC AGC GAG CTG AGG AAA GAG TAC GGA ATG ACC TAC AAT GAC TTC         382
247 Leu Ile Ser Glu Leu Arg Lys Glu Tyr Gly Met Thr Tyr Asn Asp Phe
248              115                 120                 125
250 TTC ATG GTG CTA ACA GAT GTG GAT CTG AGA GTC AAG CAA TAC TAT GAG         430
251 Phe Met Val Leu Thr Asp Val Asp Leu Arg Val Lys Gln Tyr Tyr Glu
252          130                 135                 140
254 GTA CCA ATA ACA ATG AAG TCT GTG TTT GAT CTG ATC GAT ACT TTC CAG         478
255 Val Pro Ile Thr Met Lys Ser Val Phe Asp Leu Ile Asp Thr Phe Gln
256      145                 150                 155
258 TCC CGA ATC AAA GAT ATG GAG AAG CAG AAG AAG GAG GGC ATT GTT TGC         526
259 Ser Arg Ile Lys Asp Met Glu Lys Gln Lys Lys Glu Gly Ile Val Cys
260 160                 165                 170                 175
262 AAA GAG GAA GTT GGG GGA GTG TTA GAA CTG TTC CCA ATT AAT GGG AGC         574
263 Lys Glu Glu Val Gly Gly Val Leu Glu Leu Phe Pro Ile Asn Gly Ser
264                 180                 185                 190
266 TCT GTT GTT GAG CGA GAA GAC GTA CCA GCC CAT TTG GTG AAA GAC ATT         622
267 Ser Val Val Glu Arg Glu Asp Val Pro Ala His Leu Val Lys Asp Ile
268              195                 200                 205
270 CGT AAC TAT TTT CAA GTG AGC CCG GAG TAC TTC TCC ATG CTT CTA GTC         670
271 Arg Asn Tyr Phe Gln Val Ser Pro Glu Tyr Phe Ser Met Leu Leu Val
272          210                 215                 220
274 GGA AAA GAC GGA AAT GTC AAA TCC TGG TAT CCT TCC CCA ATG TGG TCC         718
275 Gly Lys Asp Gly Asn Val Lys Ser Trp Tyr Pro Ser Pro Met Trp Ser
276      225                 230                 235
278 ATG GTG ATT GTG TAC GAT TTA ATT GAT TCG ATG CAA CTT CGG AGA CAG         766
279 Met Val Ile Val Tyr Asp Leu Ile Asp Ser Met Gln Leu Arg Arg Gln
280 240                 245                 250                 255
282 GAA ATG GCG ATT CAG CAG TCA CTG GGG ATG CGC TGC CAG AAG ATG AGT         814
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Output Set: **N:\CRF4\11292002\I884319.raw**

```
283 Glu Met Ala Ile Gln Gln Ser Leu Gly Met Arg Cys Gln Lys Met Ser
284                 260                 265                 270
286 ATG CAG GCT ATG GTT ACC ATA GTT ACC ACC AAG GAT ACC AGG ATG GTT       862
287 Met Gln Ala Met Val Thr Ile Val Thr Thr Lys Asp Thr Arg Met Val
288             275                 280                 285
290 ACC AGG ATG ACT ACC GTC ATC ATG AGA GTT ATC ACC ATG GAT ACC CTT       910
291 Thr Arg Met Thr Thr Val Ile Met Arg Val Ile Thr Met Asp Thr Leu
292         290                 295                 300
294 ACT GAG CAG AAA TAT GTA ACC TTA GAC TCA GCC AGT TTC CTC TGC AGC       958
295 Thr Glu Gln Lys Tyr Val Thr Leu Asp Ser Ala Ser Phe Leu Cys Ser
296     305                 310                 315
298 TGC TAAAACTACA TGTGGCCAGC TCCATTCTTC CACACTGCGT ACTACATTTC          1011
299 Cys
300 320
302 CTGCCTTTTT CTTTCAGTGT TTTTCTAAGA CTAAATAAAT AGCAAACTTT CACCTAAAAA   1071
304 AAAAAAAAAA AAAAAAA                                                 1088
307 (2) INFORMATION FOR SEQ ID NO: 4:
309      (i) SEQUENCE CHARACTERISTICS:
310           (A) LENGTH: 320 amino acids
311           (B) TYPE: amino acid
312           (D) TOPOLOGY: linear
314      (ii) MOLECULE TYPE: protein
316      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
318 Lys Lys Gly Gly Lys Thr Glu Gln Asp Gly Tyr Gln Lys Pro Thr Asn
319   1               5                  10                  15
321 Lys His Phe Thr Gln Ser Pro Lys Lys Ser Val Ala Asp Leu Leu Gly
322              20                  25                  30
324 Ser Phe Glu Gly Lys Arg Arg Leu Leu Leu Ile Thr Ala Pro Lys Ala
325          35                  40                  45
327 Glu Asn Asn Met Tyr Val Gln Gln Arg Asp Glu Tyr Leu Glu Ser Phe
328      50                  55                  60
330 Cys Lys Met Ala Thr Arg Lys Ile Ser Val Ile Thr Ile Phe Gly Pro
331  65                  70                  75                  80
333 Val Asn Asn Ser Thr Met Lys Ile Asp His Phe Gln Leu Asp Asn Glu
334                  85                  90                  95
336 Lys Pro Met Arg Val Val Asp Asp Glu Asp Leu Val Asp Gln Arg Leu
337             100                 105                 110
339 Ile Ser Glu Leu Arg Lys Glu Tyr Gly Met Thr Tyr Asn Asp Phe Phe
340         115                 120                 125
342 Met Val Leu Thr Asp Val Asp Leu Arg Val Lys Gln Tyr Tyr Glu Val
343     130                 135                 140
345 Pro Ile Thr Met Lys Ser Val Phe Asp Leu Ile Asp Thr Phe Gln Ser
346 145                 150                 155                 160
348 Arg Ile Lys Asp Met Glu Lys Gln Lys Lys Glu Gly Ile Val Cys Lys
349                 165                 170                 175
351 Glu Glu Val Gly Gly Val Leu Glu Leu Phe Pro Ile Asn Gly Ser Ser
352             180                 185                 190
354 Val Val Glu Arg Glu Asp Val Pro Ala His Leu Val Lys Asp Ile Arg
355         195                 200                 205
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VERIFICATION SUMMARY DATE: 11/29/2002
PATENT APPLICATION: **US/09/884,319** TIME: 16:01:33

Input Set : **N:\Crf3\RULE60\09884319.raw**
Output Set: **N:\CRF4\11292002\I884319.raw**

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]